

comparing the determined sequence to at least one sequence shown in Table 1;

classifying the mycobacteria from the extent of similarity of the compared sequences.

5. The method of claim 4, wherein at least 100 contiguous bases are determined from the target nucleic acid.

6. The method of claim 4, wherein the determined sequence is compared with at least ten sequences shown in Table 1.

7. A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid;

determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more of the highlighted positions in a sequence shown in Table 1, the identity of the one or more bases characterizing the species of mycobacteria that is present in the sample.

8. The method of claim 7, wherein the identity of at least 10 bases in the target nucleic acid at positions corresponding to highlighted positions in a sequence shown in Table 1 is determined.

9. The method of claim 8, wherein the identity of at least 20 bases in the target sequence at highlighted positions shown in Table 1 are identified.

10. The method of claim 9, further comprising comparing the 20 determined bases with 20 bases occupying corresponding positions in each of at least ten sequences from Table 1.

11. A sequence-specific polynucleotide probe or primer that hybridizes to a segment of a mycobacterial rpoB sequence shown in Table 1 or its complement without hybridizing to the M. tuberculosis sequence designated ATCC9-Mtb in Table 1 or its complement, wherein the segment includes a highlighted nucleotide position shown in Table 1.

(Amended) 12[10]. The sequence-specific polynucleotide of claim 9 that is probe.

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(Amended) 13[11]. The sequence-specific polynucleotide of claim 12[10], wherein a central position of the probe aligns with a highlighted nucleotide position shown in Tables 13.

(Amended) 14[12]. The sequence-specific polynucleotide of claim 9 that is a primer.

(Amended) 15[13]. The sequence-specific polynucleotide of claim 14[12], wherein the 3' end of the primer aligns with a highlighted nucleotide position shown in Table 13.

(Amended) 16[14]. The sequence-specific polynucleotide of claim 8 that is between 10 and 50 bases long.

(Amended) 17[19]. A computer-readable storage medium for storing data for access by an application program being executed on a data processing system, comprising:

a data structure stored in the computer-readable storage medium, the data structure including information resident in a database used by the application program and including:

a plurality of records, each record comprising information identifying a polymorphism or sequence shown in Table 1.

(Amended) 18[20]. The computer-readable storage medium of claim 17[19], wherein each record has a field identifying a base occupying a polymorphic site and a field identifying location of the polymorphic site.

(Amended) 19[21]. The computer-readable storage medium of claim 17[19], wherein each record records a contiguous segment of at least 50 bases from an rpoB sequence shown in Table 1.

(Amended) 20[22]. The computer-readable storage medium of claim 19[21], comprising at least ten records each recording a

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